

1

50

| | | |
|-----------|-----|---|
| AtBI-1 | (1) | -----MDAFSSFFDSQPGS---RSWSYDSLKNFRQISPQAVQNHLKR |
| BnBI-1 | (1) | -----MDSFSSFFDSQPGS---RSWSYDSLKNLRQISPQVQNHLKR |
| GmBI2 | (1) | ----RLQAMDAFNSFFDS----RNRWNYDTLKNFRQISPQVQNHLKQ |
| GmBI3 | (1) | ITKTIRFDLSIFSMDFKSPSSSSRSRWSYDTLKNFREISPQVQNLKL |
| HvBI-1 | (1) | -----MDAFYSTS---SAAASGWGHDSLKNFRQISPQVQSHLKL |
| NtBI-1 | (1) | -----MESCTSFFNSQSASS-RNRWNSYDSLKNFRQISPQVQTHLKK |
| OsBI-1 | (1) | -----MDAFYSTSSAYGAAASGWGYDSLKNFRQISPQVQSHLKL |
| TaBI11 | (1) | ----- |
| TaBI18 | (1) | -----FSGTFRNSRSDDFVLCELQRELPRCRDATLTV |
| TaBI5 new | (1) | -----VAMPGR |
| ZmBI14 | (1) | ----- |
| ZmBI16 | (1) | ----- |
| ZmBI33 | (1) | ----- |
| ZmBI8 | (1) | ----- |
| Consensus | (1) | F S W YDSLKN R ISP VQ HLK |

51

100

| | | |
|-----------|------|--|
| AtBI-1 | (39) | VYLTLCALVASAFGAYLHVWNIGGILTTIGCIGTMIWLLSCPPYEHQK |
| BnBI-1 | (39) | VYLTLCALVASAFGAYLHVWNIGGILTTIGCFGSMIWLLSCPPYEQQK |
| GmBI2 | (40) | VYFTLCFAVVAAAAGAYLHVLLNIGGFLTTACMGSSFWLSTPPFEERK |
| GmBI3 | (51) | VYFTLCACVAAAAGAYLHVWNIGGFLTLASIGSMFWLLSTPPFEEQK |
| HvBI-1 | (37) | VYLTLCFALASSAVGAYLHIALNIGGMLTMLACVTIAWMFSVPVYEERK |
| NtBI-1 | (41) | VYLSLCALVASAAGAYLHILWNIGGLLTLGCVGSIVWLMATPLYEEQK |
| OsBI-1 | (40) | VYLTLCVALAASAVGAYLHVNLNIGGMLTMLGCVGSIAWLFSVPVFEERK |
| TaBI11 | (1) | ----- |
| TaBI18 | (33) | VYVIPIVGRIKSAAGAYLHIALNIGGMLTMLACIGTIAWMFSPVYEERK |
| TaBI5 new | (7) | RFRLYALPGLICRGCLPAHCPEHWRDADNARVYRNHRLDVLGASLRGE |
| ZmBI14 | (1) | -----GSIAWLFSPVYEERK |
| ZmBI16 | (1) | -----WNIGVRLTMLGCIGSIDWLFSVPVYEERK |
| ZmBI33 | (1) | -----WNIGGTLTMLGCVGSIAWLFSPVYEERK |
| ZmBI8 | (1) | ----- |
| Consensus | (51) | VY TLC AL ASA GAYLHV NIGG LT LGCIGSI WL S PVYEERK |

101

150

| | | |
|-----------|-------|--|
| AtBI-1 | (89) | RLSLLFVSAVLEGASVGPLIKVAIDVDP SILITAFVGT AIAFVCFSAAAM |
| BnBI-1 | (89) | RLSLLFLSAVLEGASVGPLIKVAVDFDPSILITAFVGT AIAFICFSGAAM |
| GmBI2 | (90) | RTVLLMAASLFGSSIGPLIDLAHIDPSLIFSAFVGT AIAFACFSGAAL |
| GmBI3 | (101) | RLSLLMASALFGASIGPLIDLAFAIDPGLIIGAFVATSLAFACFSVAL |
| HvBI-1 | (87) | RFGLLMGAALLEGASVGPLIELAIDFDPSILVTGFVGT AIAFGCFSGAAI |
| NtBI-1 | (91) | RIALLMAAALFKGASIGPLIELAIDFDPSIVIGAFVGCAVAFGCFSAAM |
| OsBI-1 | (90) | RFGILLAAALLEGASVGPLIKLAVDFDSSILVTAFVGT AIAFGCFTCAA |
| TaBI11 | (1) | -----AAI |
| TaBI18 | (83) | RFGLLMGAALLEGASVGPLIELAIDFDPSILVTGFVGT AIAFGCFSGAAI |
| TaBI5 new | (57) | EVWAADGCSLLEGASVGPLIELAIDFDPSILVTGFVGT AIAFGCFSGAAI |
| ZmBI14 | (17) | RYWLLMAAALLEGASVGPLIKLAVEFDPSILVTAFVGT AIAFACFSCAAM |
| ZmBI16 | (30) | RYGLLMAAALLEGASVGPLVKLAVEFDPSILVTAFVGT AIAFACFSGAAM |
| ZmBI33 | (30) | RYGLLMAAALLEGASVGPLVKLAVEFDPSILVTAFVGT AIAFACFSGAPW |
| ZmBI8 | (1) | -----VIDLDSRILVTAFVGT AIAFACFSGAAI |
| Consensus | (101) | R LLMAAALLEGASVGPLI LAIDFDPSILVTAFVGT AIAFACFSGAAI |

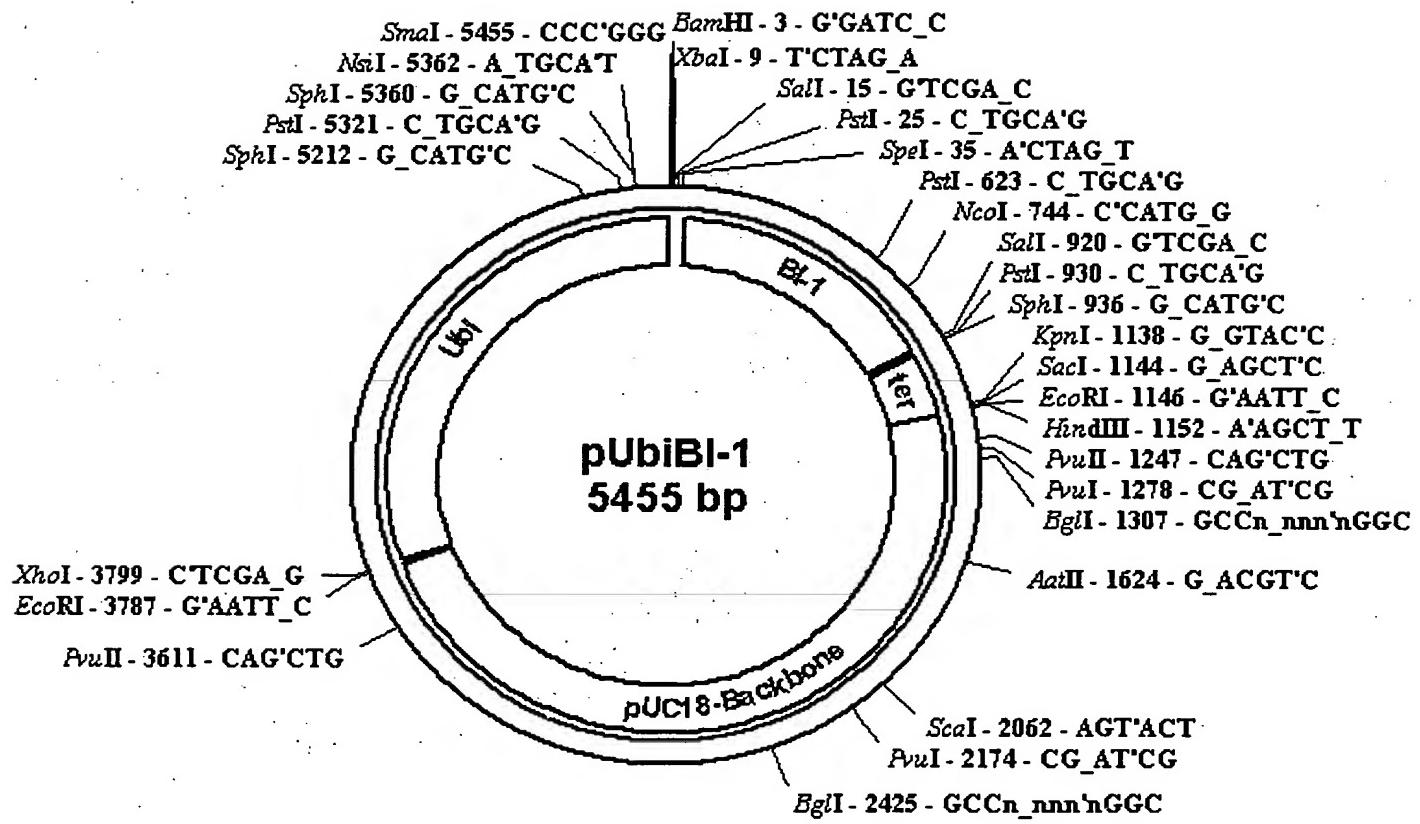
Fig.1a

| | | | |
|-----------|-------|---|-----|
| | | 151 | 200 |
| AtBI-1 | (139) | LARRREYLYLGGLLSSGLSMLWLQFASSIFG-GSASIFKFELYFGLLIF | |
| BnBI-1 | (139) | LARRREYLYLGGLLSSGLSMLWLQFASSIFG-GSASIFKFELYFGLLIF | |
| GmBI2 | (140) | VARRREYLYLGGLVSSGLSILLWLHFASSIFG-GSTALFKFELYFGLLVF | |
| GmBI3 | (151) | VARRREYLYLGGLLSSWLSILMWLHSDSSLFG-GSIALFKFELYFGLLVF | |
| HvBI-1 | (137) | IAKRREYLYLGGLLSSGLSILLWLQFVTSIFGHSS-GSFMFEVYFGLLIF | |
| NtBI-1 | (141) | VARRREYLYLGGLLSSGLSILFWLHFASSIFG-GSMALFKFEVYFGLLVF | |
| OsBI-1 | (140) | VAKRREYLYLGGLLSSGLSILLWLQFAASIFGHST-GSFMFEVYFGLLIF | |
| TaBI11 | (4) | IAKRREYLYLGGLLSSGLSILLWLQFATSIFGHSS-GSFMFEVYFGLLIF | |
| TaBI18 | (133) | IAKRREYLYLGGLLSSG-----LTIL | |
| TaBI5 new | (107) | IAKRREYLYLGGLLSSGLSILLWLQFATSIFGHSS-GSFMFEVYFGLLIF | |
| ZmBI14 | (67) | VAKRREYLYLGGLLSSGLSILLWLQFAASIFGHQSTSSFMFEVYFGLLIF | |
| ZmBI16 | (80) | VARRREYLYLGGLLSSGLSILLWLQLAASIF-GHSATSFMFEVYFGLLIF | |
| ZmBI33 | (80) | WQAR-EYLYLGGSRRGSPSCSGCSSPPPSS--ALRNSFMFEVYFGLLIL | |
| ZmBI8 | (29) | IAKRREYLYLGGLLSSGLSILLWLQFATSIFGHTS-ATFMFELYFGLLVF | |
| Consensus | (151) | VAKRREYLYLGGLLSSGLSILLWLQFASSIFG S ASFMFEVYFGLLIF | |
| | | 201 | 250 |
| AtBI-1 | (188) | VGYMVVDTQEIIIEKAHLGMDYVKHSLTLFTDFVAVFVRILIIMLKNSAD | |
| BnBI-1 | (188) | VGYMVVDTQDIIIEKAHLGMDYVKHSLTLFTDFVAVFVRVLIIIMLKNSAD | |
| GmBI2 | (189) | VGYIVVDTQEIERAHLGLDYVKHALTLFTDLAAIFVRILIIMLKNSTE | |
| GmBI3 | (200) | VGYVIVDTQEIIERAHFGDLDYVKHALTLFTDLAAIFVRILIIMLKNSSE | |
| HvBI-1 | (186) | LGYMVYDTQEIIERAHGDMDYIKHALTLFTDFVAVLVRVLIIIMLKNA GD | |
| NtBI-1 | (190) | VGYIIFDTQDIIIEKAHLGLDYVKHALTLFTDFVAVFVRILIIMLKNASD | |
| OsBI-1 | (189) | LGYMVYDTQEIIERAHGDMDYIKHALTLFTDFVAVLVRILVIMLKNA SD | |
| TaBI11 | (53) | LGYMVYDTQEIIERAHGDMDYIKHALTLFTDFVAVLVRILIIMLKNA GD | |
| TaBI18 | (154) | L----- | |
| TaBI5 new | (156) | LGYMVYDTQEIIERAHGDMDYIKHALTLFTDFVAVLVRVLIIIMLKNA AD | |
| ZmBI14 | (117) | LGYMVYDTQEVIERAHHG----- | |
| ZmBI16 | (129) | LGYVVYDT----- | |
| ZmBI33 | (127) | LG----- | |
| ZmBI8 | (78) | LGYMFDTQEIIERAHRGDMDYIKHALTLFTDFVAVLVRILVIMMKNA QE | |
| Consensus | (201) | LGYMVYDTQEIIERAH GDMDYIKHALTLFTDFVAV VRILIIMLKNA D | |
| | | 251 | 300 |
| AtBI-1 | (238) | KEEKKKKRRN-----GDVK-I-LYGCYRVWPL-RYYLLALSIGDQTCF | |
| BnBI-1 | (238) | KEDKKKKRRN----D-KVRKKAK-SGCVCFKK-----KRVG | |
| GmBI2 | (239) | RNEKKKKRRD----- | |
| GmBI3 | (250) | RNEKKKKRRD--ADRPTRAQASLQ-FSLWRIHN-----LFR-CWSLV- | |
| HvBI-1 | (236) | KSEDKKKRKRG-----S----- | |
| NtBI-1 | (240) | KEEKKKKRRN---CISGYSKTL-L-NLAFSCS---TSVDLRQVCC--FG | |
| OsBI-1 | (239) | KSEEKKRKRS-ELLFPLCT-EKTTAAIASTYYDRAALQLGF MVNTSSFA | |
| TaBI11 | (103) | KSEDKKKRKRRS----- | |
| TaBI18 | (155) | ----- | |
| TaBI5 new | (206) | KVGGQEEEEKS----- | |
| ZmBI14 | (135) | ----- | |
| ZmBI16 | (137) | ----- | |
| ZmBI33 | (129) | ----- | |
| ZmBI8 | (128) | KSQDEKKRK----- | |
| Consensus | (251) | K E KKKR | |

Fig. 1b

| | | |
|-----------|---|----------------------|
| | 301 | |
| AtBI-1 | (278) H-KG-SACFTSAQVPSSDCK----- | LECCSSFHKLLFFKSL |
| BnBI-1 | (269) VISTDMIALVFFT CLEQFW----- | QHTLRICVFLLVTPDCEWI |
| GmBI2 | (249) ----- | |
| GmBI3 | (288) LVSYVFAVMVNVRISFKHLHMYLPIS-CVV-HHTLV-KKKKKKKKKKKKK | |
| HVBI-1 | (248) ----- | |
| NtBI-1 | (279) NASD-AARLCYAAQCQCGYGGT-MVLF----PKHTIK-HACLHYIDNLRVY | |
| OsBI-1 | (287) FC-YGVNLLRFVVVVALQILACYMTRIFL-WWSR-SKRENTSSFATNLFA | |
| Consensus | (301) | |
| | 351 | 400 |
| AtBI-1 | (312) VLLIASYQAKNNVGK----- | SCLNFLKCVHFRKKKKKKKK |
| BnBI-1 | (307) SILKLC-KLSVGS----- | |
| GmBI2 | (249) ----- | |
| GmBI3 | (335) KKKKKXXXXXXXXXXXX--XXXXXGVCGLRYSRHSSNH-EGSLW-PGLC- | |
| HVBI-1 | (248) ----- | |
| NtBI-1 | (322) YLFLLPFAVLGCS-LYS-FSVMLDHLLS-RLISHIDGRNENSHRRPNLFK | |
| OsBI-1 | (334) FW-LMMILSPKKKK----- | |
| Consensus | (351) | |
| | 401 | 450 |
| AtBI-1 | (348) ----- | |
| BnBI-1 | (319) ----- | |
| GmBI2 | (249) ----- | |
| GmBI3 | (380) ACIDTVH-FGCNL CANS-YNVE-FI-EK-EEEEERLIG-PIAMCRVIWFV | |
| HVBI-1 | (248) ----- | |
| NtBI-1 | (369) TEAQL----- | |
| Consensus | (401) | |
| | 451 | 500 |
| GmBI3 | (424) ENT-LAV-KLLVPLCS--LAMCLL-W-MSGFLLNIFICIC--S-YIV-TS | |
| Consensus | (451) | |
| | 501 512 | |
| GmBI3 | (464) FLGLKKEKKKKK | |
| Consensus | (501) | |

Fig.1c

**Fig. 2**

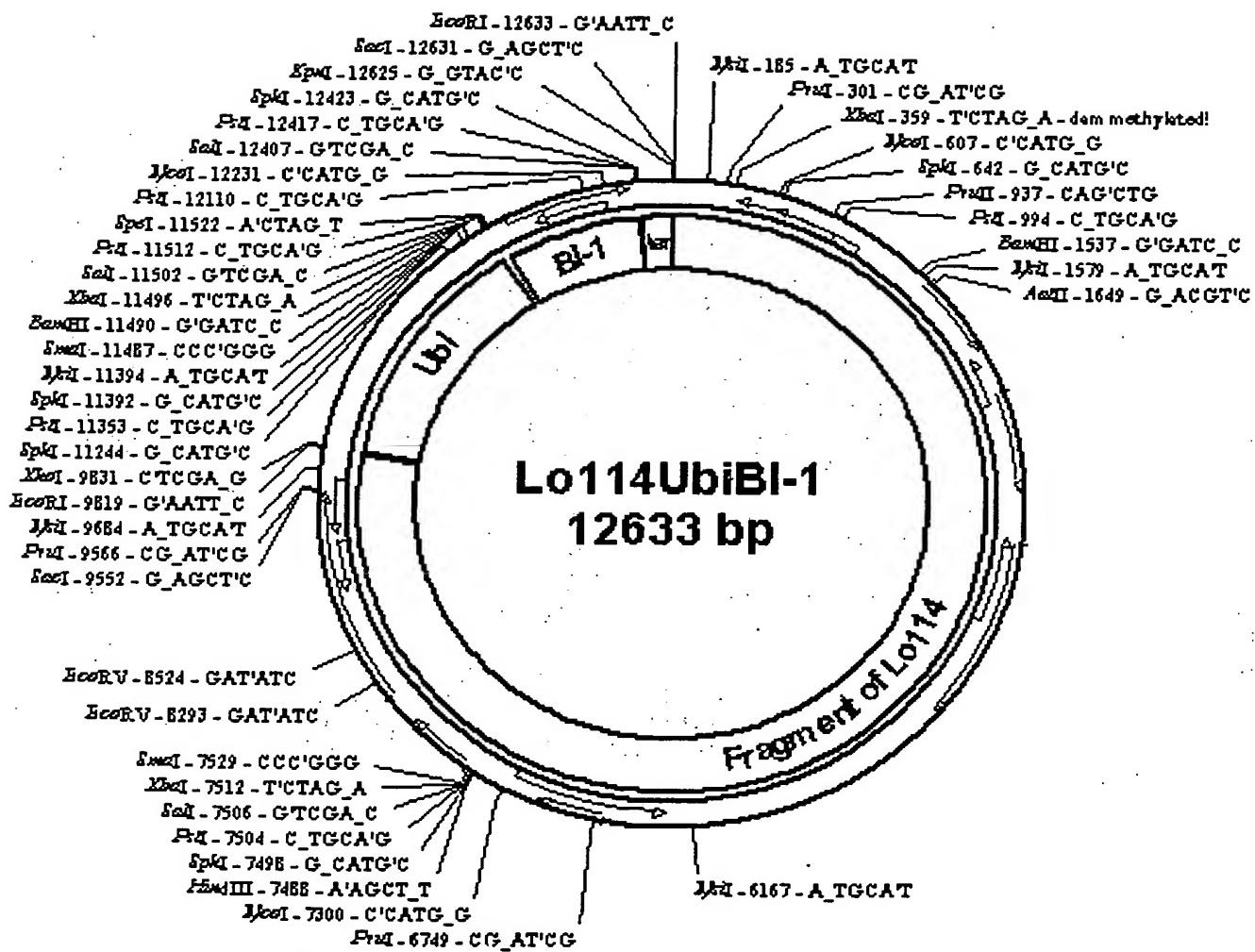


Fig. 3

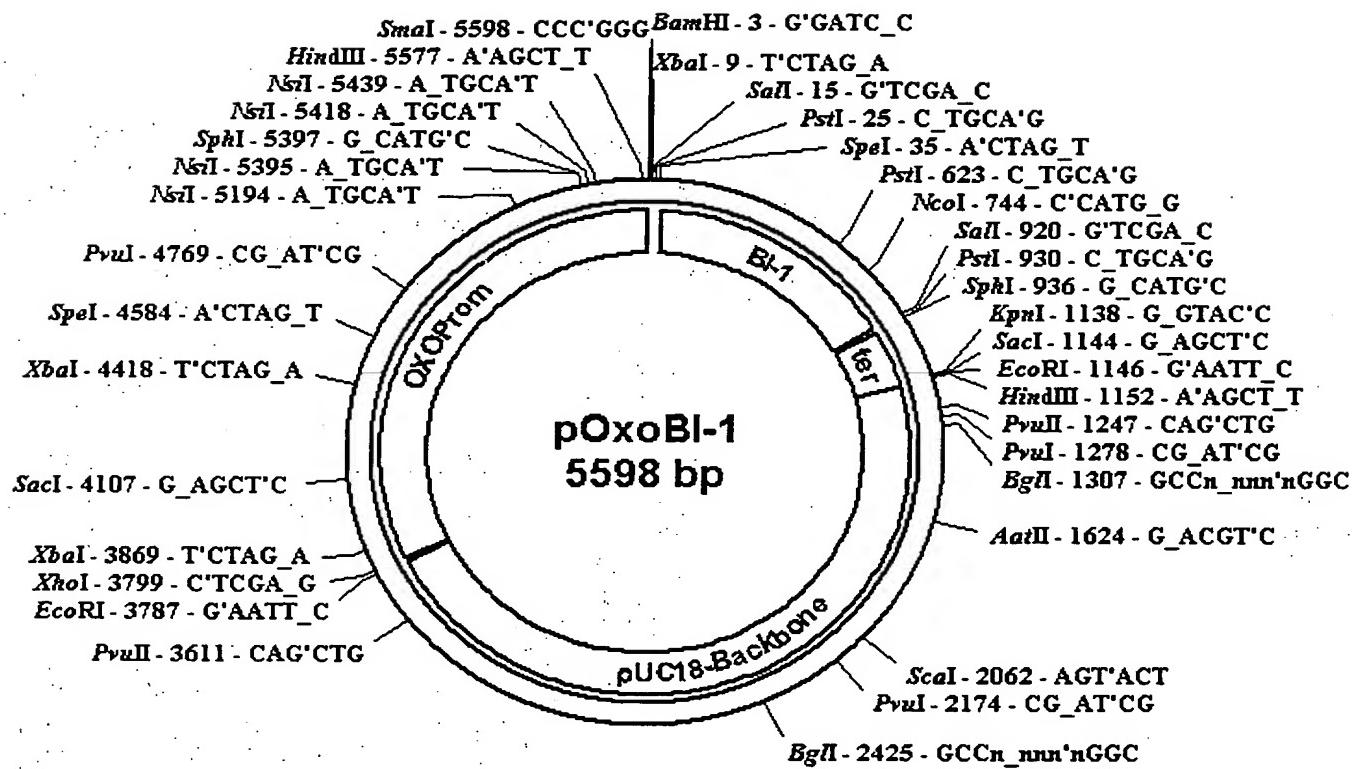
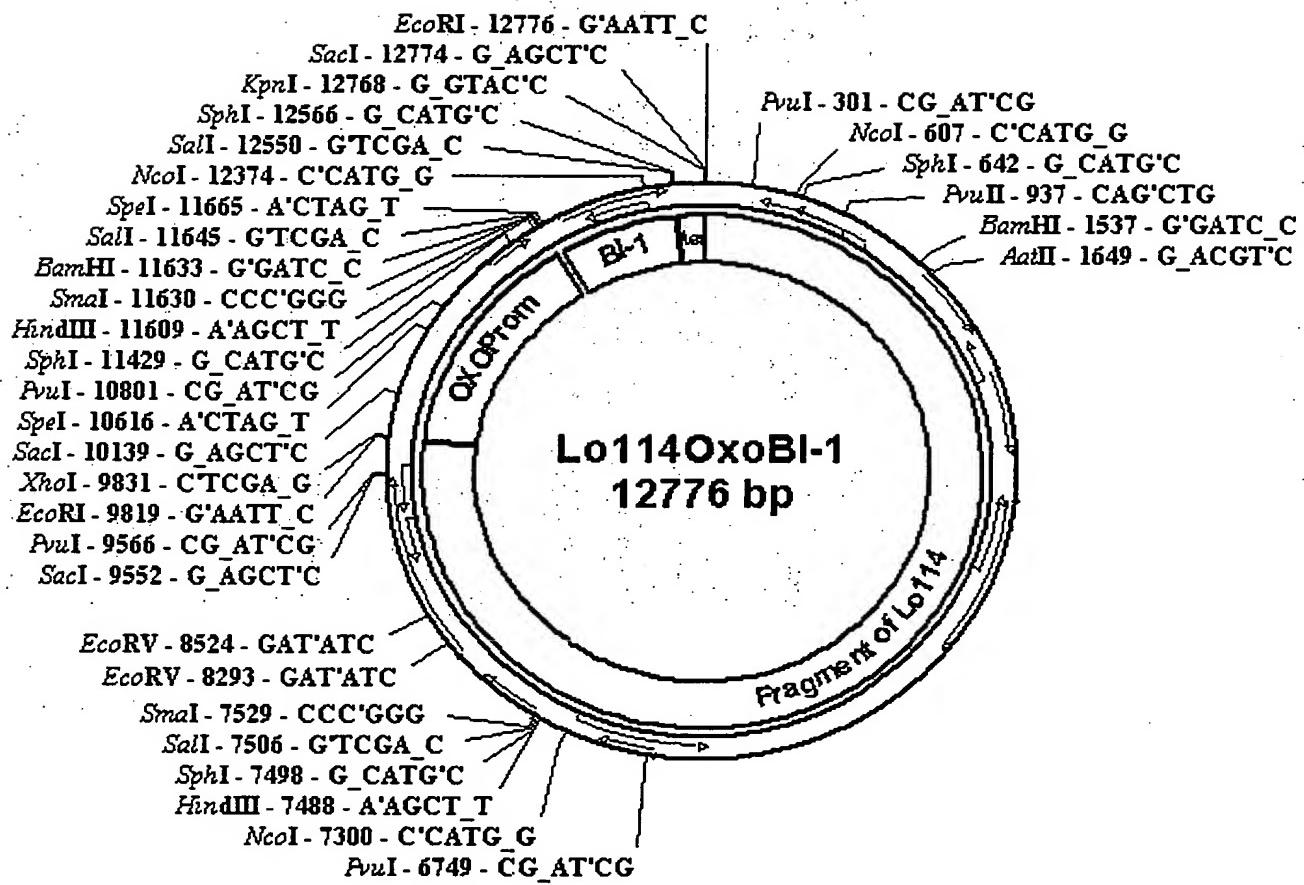


Fig. 4

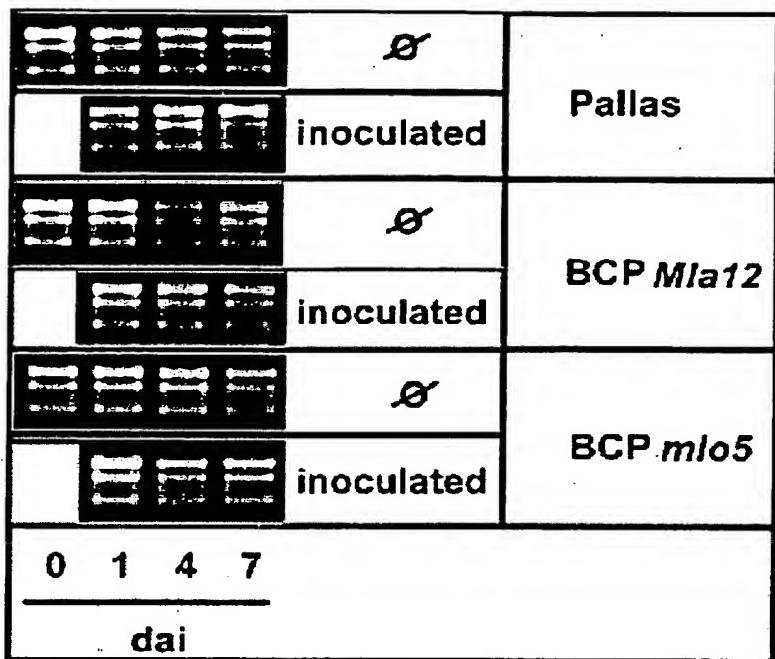
**Fig.5**

| | | |
|----------------|---|-----|
| <i>H. vul.</i> | MDFYSTSS---AAASGWGHDSLKNFRQISPAVQSHLKLVYLTLCFALASSAVGAYLHIA | 57 |
| <i>O. sat.</i> | MDFYSTSSAYGAAASGWGYDSLKNFRQISPAVQSHLKLVYLTLCVALAASAVGAYLHVA | 60 |
| <i>A. tha.</i> | MDFSSFFDS-QPGSRSTSYDSLKNFRQISPAVQNLKRVYETLCCALVASAFGAYLHVL | 59 |
| <i>H. sap.</i> | MNIFDRKIN-----FLALLKESHTIPSTOQHLKKVASFALCMFVAAGAYWHMV | 50 |
| <i>H. vul.</i> | LN--IGGELTMLACVGTLIAWMFSVPVYEE--RKRFGLLMGARLEGASVGPLIELAIDFD | 113 |
| <i>O. sat.</i> | LN--IGGELTMLGCVGSIAWLFSPVPFEE--RKRFGILLAMLEGASVGPLIKLAVDFD | 116 |
| <i>A. tha.</i> | WN--IGGILTTIGCIGTMIWLLSCPPYEH--QKRLSLLFVSAVLEGASVGPEIKVAIDVD | 115 |
| <i>H. sap.</i> | THFIQAGLISALGSLILMILMLATPHSHETEOKRLGLLAGFAGFLTCVGLGPALFCIAVN | 110 |
| <i>H. vul.</i> | PSILVTGFVGTIAFGCFSGAIIAKRREYLYLGGLLSSGLSILLWLQFVTSIFGHSGS | 173 |
| <i>O. sat.</i> | SSILVTAFVGTLIAFGCFTCAPIVAKRREYLYLGGLLSSGLSILLWLQFAASIFGHSTGS | 176 |
| <i>A. tha.</i> | PSILITAFVGTLIAFVCFSAAAMLAFRREYLYLGGLLSSGLSMILWLQFASSIFGGSASI | 175 |
| <i>H. sap.</i> | PSILPIAFMGTMIMIFCFILSELVYARRESYFLGGIIMSALSLLLSSSLGNVFEG-SIWP | 169 |
| <i>H. vul.</i> | FMFEVVFGLLIFLGYHVYDTQEIIIEAHGDMDYIKHALTLFTDFVAVLVRVLIIIMLKNA | 233 |
| <i>O. sat.</i> | FMFEVVFGLLIFLGYHVYDTQEIIIEAHGDMDYIKHALTLFTDFVAVLVRILVIMLKNA | 236 |
| <i>A. tha.</i> | FKFELYFGLLIFVGYHVYDTQEIIIEKAHLGDMDYVKHSLLFTDFVAVFVRILIIMLKNS | 235 |
| <i>H. sap.</i> | FQANLYVGLVVVMCGFVLVDTQLIIIEKAEGDQDYIWHCIDLFLDFITDFRKLMMILAKNE | 229 |
| <i>H. vul.</i> | GDKSEDKKKRKRGs | 247 |
| <i>O. sat.</i> | SDKSEEKKRKRS- | 249 |
| <i>A. tha.</i> | ADK-EKKKKRKN- | 247 |
| <i>H. sap.</i> | KDK---KKEKK--- | 237 |

Fig. 6

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rRNAs



BI-1

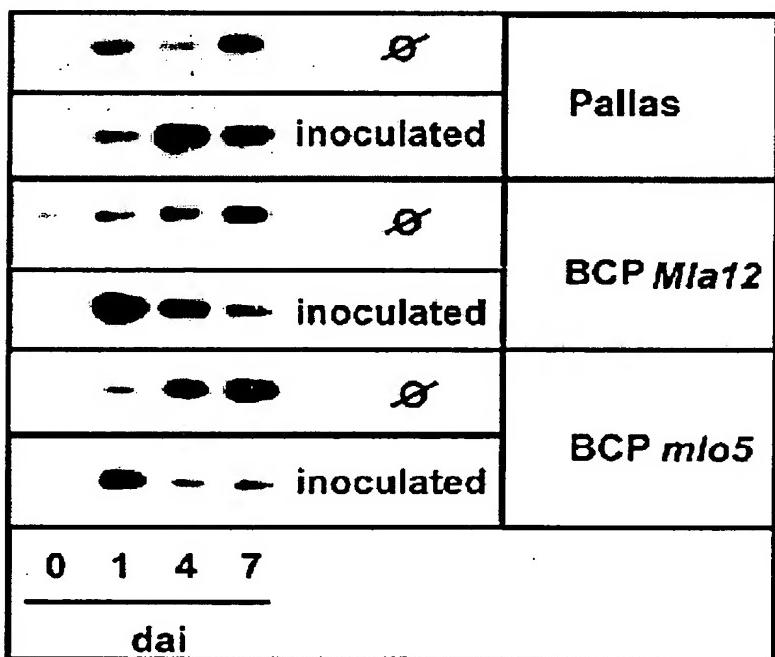


Fig. 7

23/5 48748

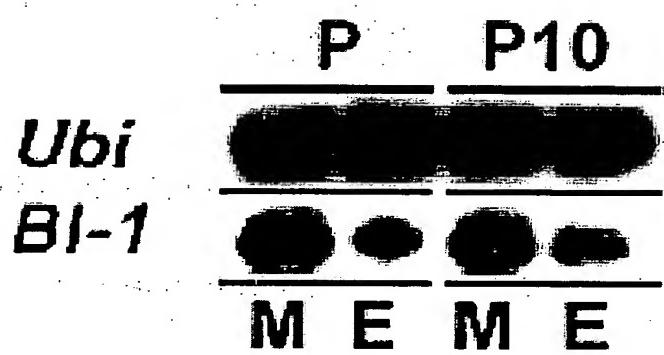


Fig. 8

10/5 48748

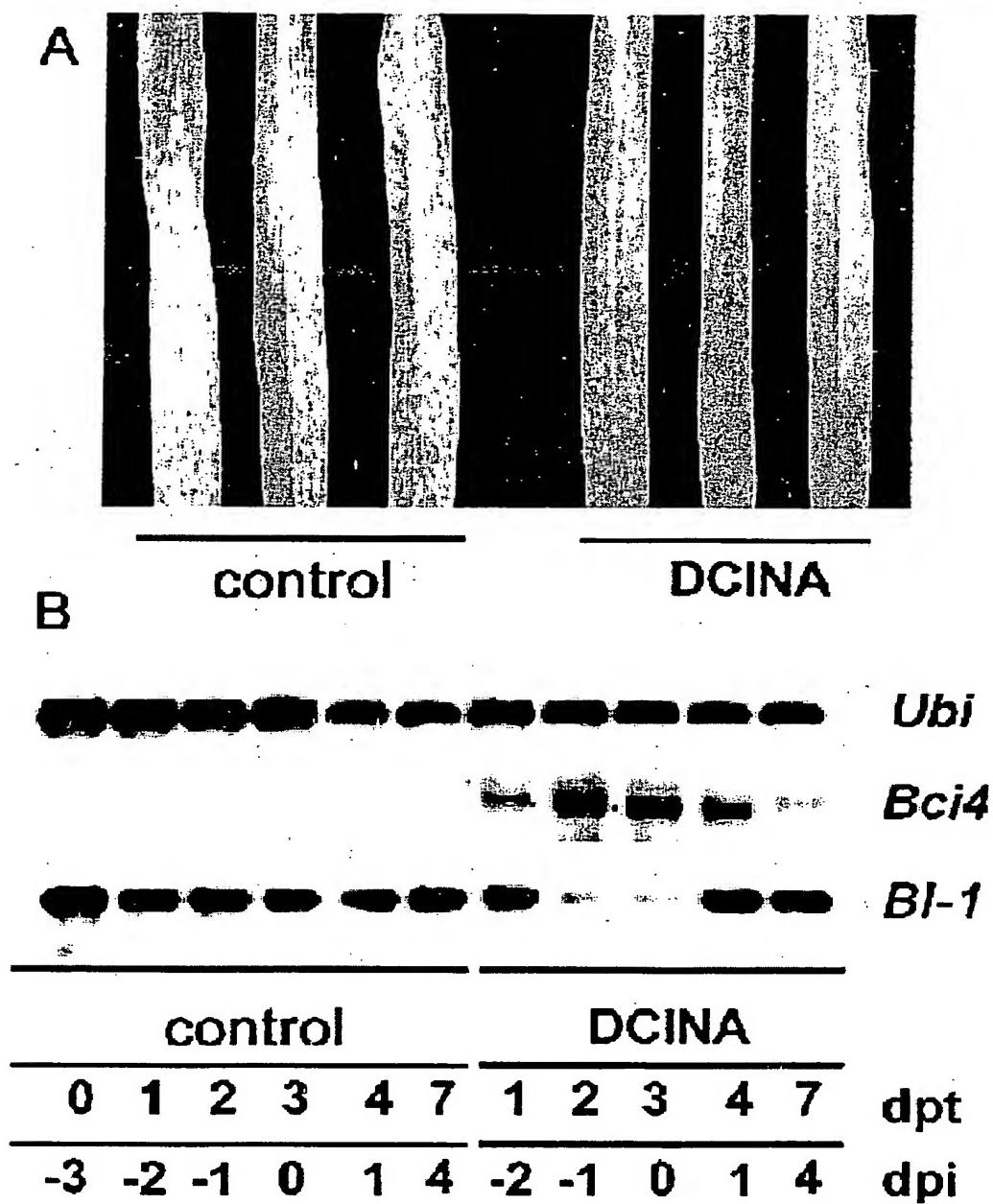


Fig. 9

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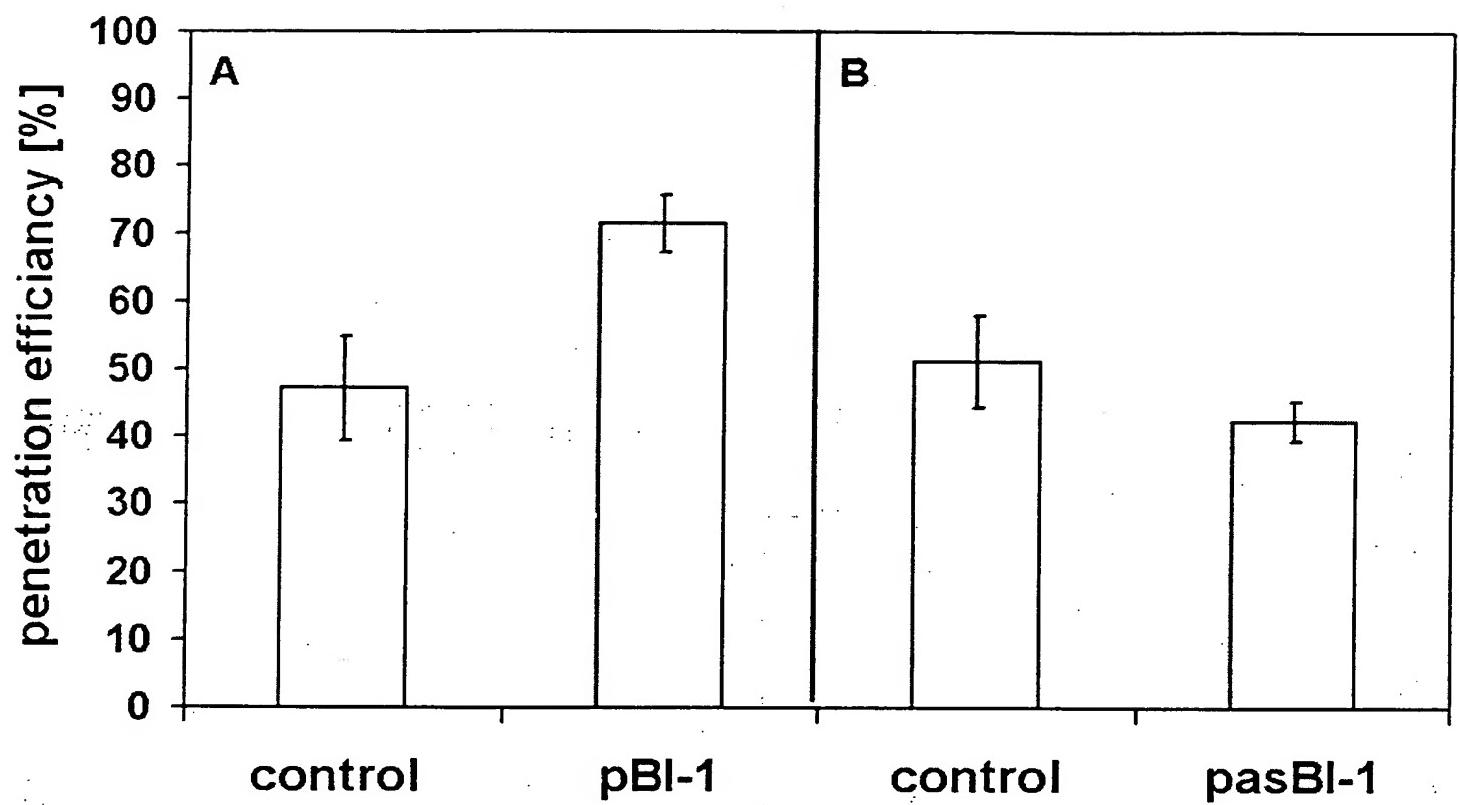


Fig.10

10/15 48748

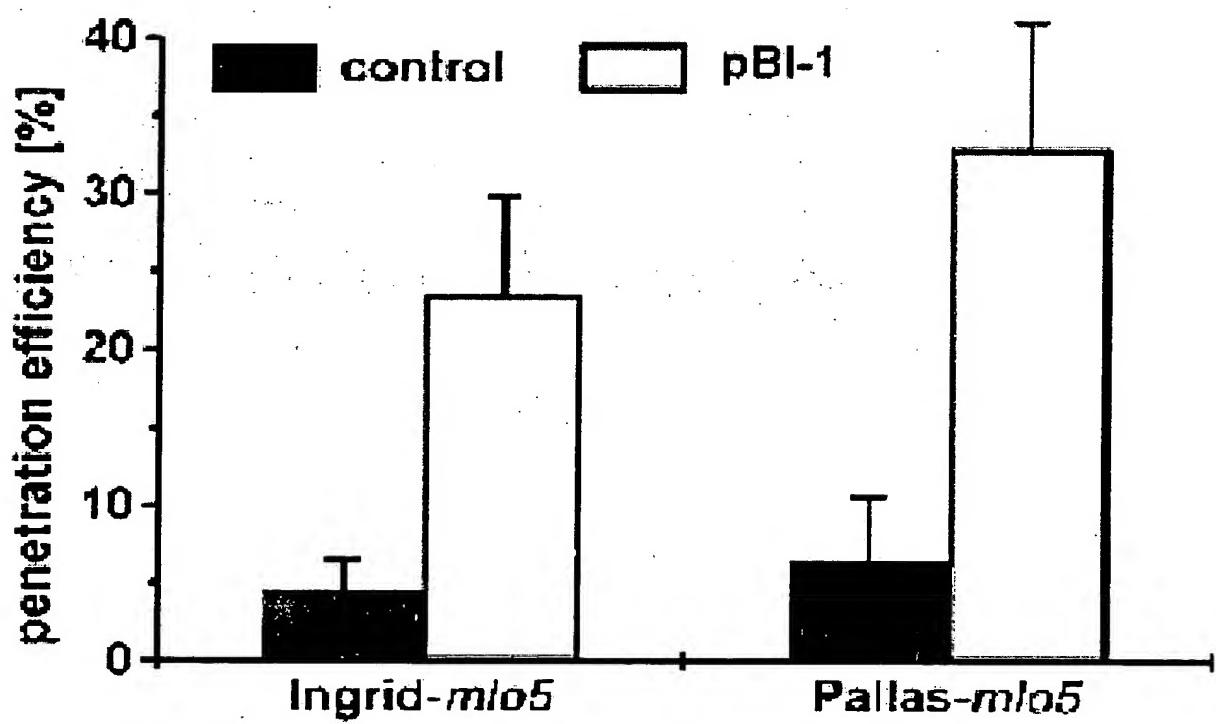


Fig.11

10/5 48748

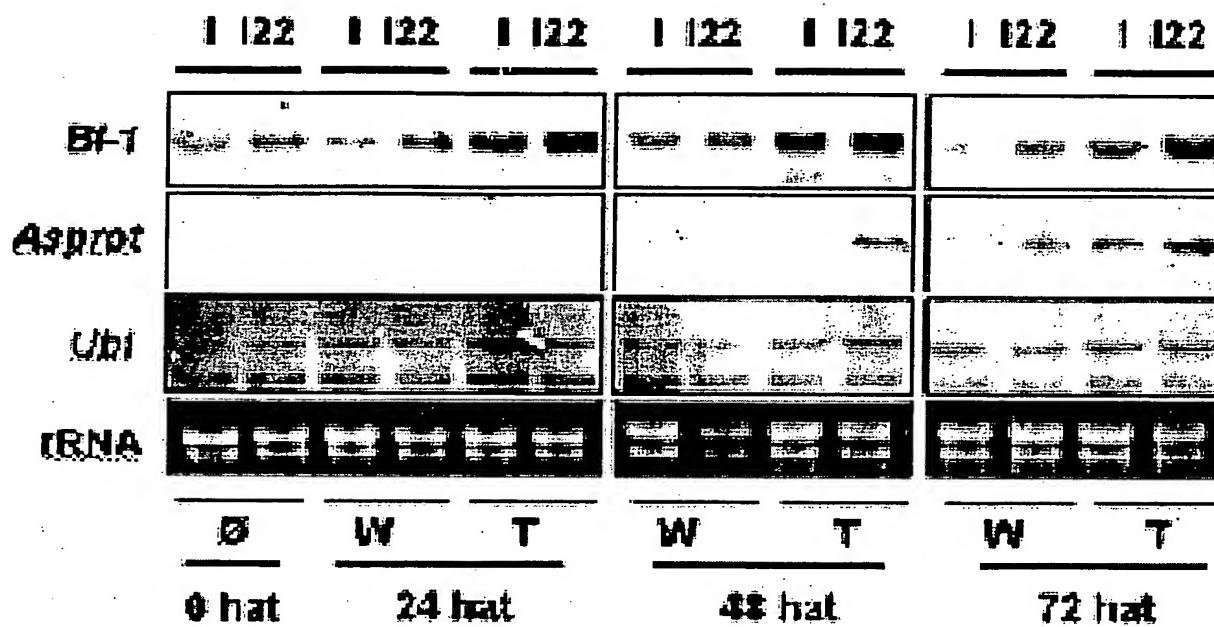


Fig.12

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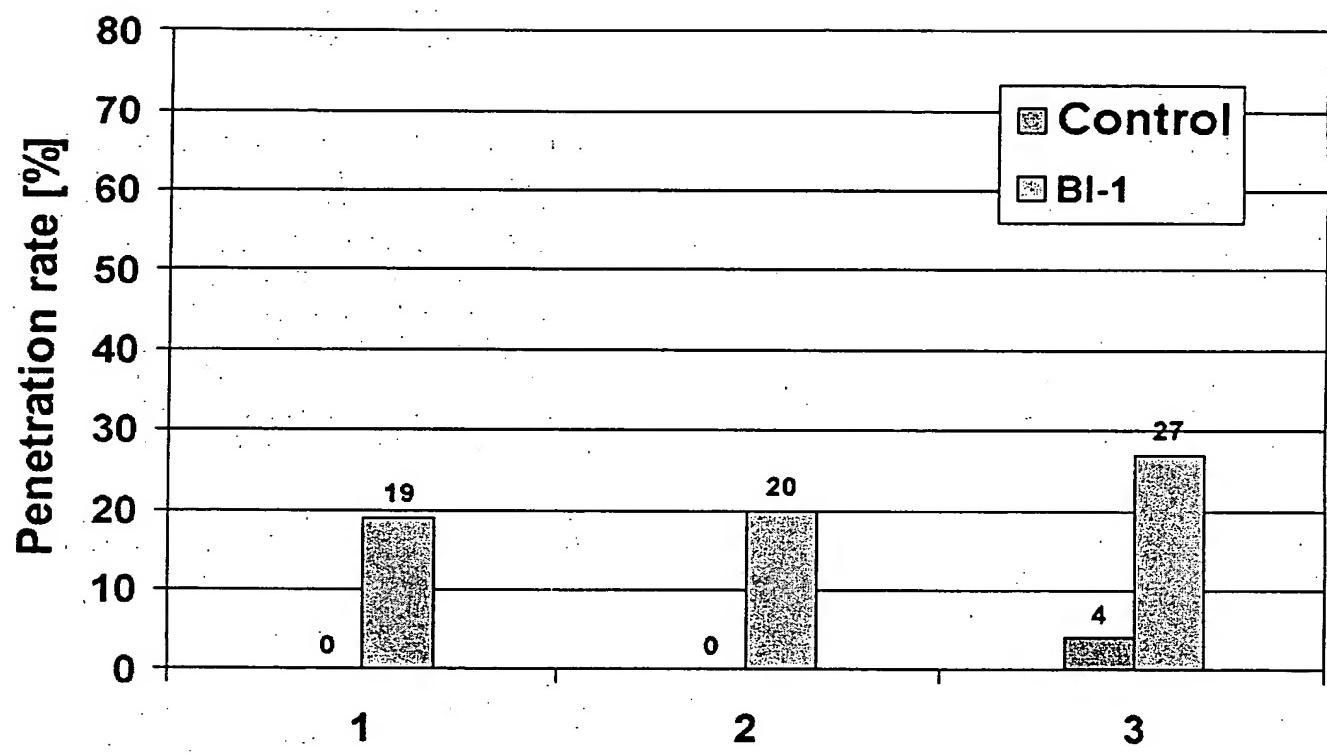


Fig.13